STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/590,886
Source: IFW
Date Processed by STIC: 9/6/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED **SUGGESTED CORRECTION** **SERIAL NUMBER:** 10/590,886

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	Invalid Line Length	The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
3	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
4	Non-ASCII	The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
5	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
7	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
8	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence. <210> sequence id number <400> sequence id number 000
9	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
10	Invalid <213> Response	Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
11	Use of <220>	Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
12	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13	Misuse of n/Xaa	"n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid

IFW

RAW SEQUENCE LISTING DATE: 09/06/2006
PATENT APPLICATION: **US/10/590,886** TIME: 10:15:46

Input Set : **E:\DJKIM.GENO.PT2.ST25.txt**
Output Set: **N:\CRF4\09062006\J590886.raw**

3 <110> APPLICANT: Genomine, Inc.
4 Korea Research Institute of Chemical Technology
6 <120> TITLE OF INVENTION: Polypeptide Having Function of Cinnamyl Alcohol Dehydrogenase, a
7 Polynucleotide Coding the Polypeptide and Those Uses
9 <130> FILE REFERENCE: DJKIM.GENO.PT2
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/590,886
C--> 11 <141> CURRENT FILING DATE: 2006-08-25
11 <150> PRIOR APPLICATION NUMBER: PCT/KR2005/000454
12 <151> PRIOR FILING DATE: 2005-02-18
14 <150> PRIOR APPLICATION NUMBER: 10-2004-0013086
15 <151> PRIOR FILING DATE: 2004-02-26
17 <160> NUMBER OF SEQ ID NOS: 6
19 <170> SOFTWARE: PatentIn version 3.3
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1205
23 <212> TYPE: DNA
24 <213> ORGANISM: Arabidopsis thaliana
26 <400> SEQUENCE: 1

see pp 2-3

Does Not Comply
Corrected Diskette Needed

27 acgcattcgt catttggtcc ctccacttag agagaagcag acagaacata actaaaatcg 60
29 agaaaaatgg caaacagtgg tgaaggtaaa gtggtgtgtg taacaggagc ctccggttac 120
31 atcgcctcat ggctcgtcaa gttcctactt agccgtggct acactgttaa ggcctccgtc 180
33 cgtgatccca gtgatccgaa aaagacacaa cacttagttt cactagaagg tgcaaaggaa 240
35 agacttcact tgttcaaagc agacctttg gaacaaggtt ctttcgactc tgctattgat 300
37 ggttgccatg gagttttcca cactgcttct ccatttttta atgatgccaa agacccacag 360
39 gctgaactta ttgatcctgc ggtcaagggg acgcttaacg ttttgaattc gtgcgccaaa 420
41 gcctcttcgg ttaagagggt tgttgtaacc tcctccatgg ctgccgttgg ttacaatgga 480
43 aaaccacgca cacctgatgt taccgtcgat gaaacttggt tctctgatcc tgagctttgc 540
45 gaggcctcca agatgtggta tgttctatcc aagactttgg cggaagatgc agcttggaaa 600
47 ctcgctaaag agaaaggctt agacattgtt actattaacc cggctatggt gatcggtcct 660
49 ctcctacagc caactctgaa cacgagtgct gctgctatat taaacttaat caatggtgca 720
51 aagactttcc caaacttgag tttcggatgg gttaatgtaa aagacgtagc caatgcgcac 780
53 atccaaacat ttgaggtccc ttcagctaat gggcgttatt gtttggtcga gcgtgtcgtt 840
55 caccactccg agattgttaa cattctacgt gagctttacc caaatctccc actacctgaa 900
57 aggtgtgtgg acgagaatcc ctacgtgcca acgtatcaag tgtccaagga taaaacgagg 960
59 agccttggca tagactacat acccttgaag gttagcatca aggagaccgt cgagtccttg 1020
61 aaggaaaaag gtttcgcaca gttctgagaa agcatttgag ccaatggatt taatccagat 1080
63 tagataaagt atttggaaga ctatttcaaa aataatattt ggaacatgtc aatgttctca 1140
65 aggagatatt agtatgttct tgtgtacttt attgttgttc catcaaatga gttacttttc 1200
67 ctttt 1205
70 <210> SEQ ID NO: 2
71 <211> LENGTH: 326
72 <212> TYPE: PRT
73 <213> ORGANISM: Arabidopsis thaliana

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75 <400> SEQUENCE: 2
77 Met Ala Asn Ser Gly Glu Gly Lys Val Val Cys Val Thr Gly Ala Ser
78 1 5 10 15
81 Gly Tyr Ile Ala Ser Trp Leu Val Lys Phe Leu Leu Ser Arg Gly Tyr
82 20 25 30
85 Thr Val Lys Ala Ser Val Arg Asp Pro Ser Asp Pro Lys Lys Thr Gln
86 35 40 45
89 His Leu Val Ser Leu Glu Gly Ala Lys Glu Arg Leu His Leu Phe Lys
90 50 55 60
93 Ala Asp Leu Leu Glu Gln Gly Ser Phe Asp Ser Ala Ile Asp Gly Cys
94 65 70 75 80
97 His Gly Val Phe His Thr Ala Ser Pro Phe Phe Asn Asp Ala Lys Asp
98 85 90 95
101 Pro Gln Ala Glu Leu Ile Asp Pro Ala Val Lys Gly Thr Leu Asn Val
102 100 105 110
105 Leu Asn Ser Cys Ala Lys Ala Ser Ser Val Lys Arg Val Val Val Thr
106 115 120 125
109 Ser Ser Met Ala Ala Val Gly Tyr Asn Gly Lys Pro Arg Thr Pro Asp
110 130 135 140
113 Val Thr Val Asp Glu Thr Trp Phe Ser Asp Pro Glu Leu Cys Glu Ala
114 145 150 155 160
117 Ser Lys Met Trp Tyr Val Leu Ser Lys Thr Leu Ala Glu Asp Ala Ala
118 165 170 175
121 Trp Lys Leu Ala Lys Glu Lys Gly Leu Asp Ile Val Thr Ile Asn Pro
122 180 185 190
125 Ala Met Val Ile Gly Pro Leu Leu Gln Pro Thr Leu Asn Thr Ser Ala
126 195 200 205
129 Ala Ala Ile Leu Asn Leu Ile Asn Gly Ala Lys Thr Phe Pro Asn Leu
130 210 215 220
133 Ser Phe Gly Trp Val Asn Val Lys Asp Val Ala Asn Ala His Ile Gln
134 225 230 235 240
137 Ala Phe Glu Val Pro Ser Ala Asn Gly Arg Tyr Cys Leu Val Glu Arg
138 245 250 255
141 Val Val His His Ser Glu Ile Val Asn Ile Leu Arg Glu Leu Tyr Pro
142 260 265 270
145 Asn Leu Pro Leu Pro Glu Arg Cys Val Asp Glu Asn Pro Tyr Val Pro
146 275 280 285
149 Thr Tyr Gln Val Ser Lys Asp Lys Thr Arg Ser Leu Gly Ile Asp Tyr
150 290 295 300
153 Ile Pro Leu Lys Val Ser Ile Lys Glu Thr Val Glu Ser Leu Lys Glu
154 305 310 315 320
157 Lys Gly Phe Ala Gln Phe
158 325
161 <210> SEQ ID NO: 3
162 <211> LENGTH: 35
163 <212> TYPE: DNA
164 <213> ORGANISM: Sense Primer
166 <400> SEQUENCE: 3
167 aaggatccat ggcaaacagt ggtgaaggta aagtg 35

invalid - see item 10 on Error Summary Sheet

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Input Set : **E:\DJKIM.GENO.PT2.ST25.txt**
Output Set: **N:\CRF4\09062006\J590886.raw**

170 <210> SEQ ID NO: 4
171 <211> LENGTH: 35
172 <212> TYPE: DNA
173 <213> ORGANISM: Antisense Primer
175 <400> SEQUENCE: 4
176 cgaagctttc agaactgtgc gaaacctttt tcctt 35
179 <210> SEQ ID NO: 5
180 <211> LENGTH: 31
181 <212> TYPE: DNA
182 <213> ORGANISM: Sense Primer
184 <400> SEQUENCE: 5
185 gaagatctca gaactgtgcg aaacctttt c 31
188 <210> SEQ ID NO: 6
189 <211> LENGTH: 29
190 <212> TYPE: DNA
191 <213> ORGANISM: Antisense Primer
193 <400> SEQUENCE: 6
194 gctctagatg gcaaacagtg gtgaaggta 29

VERIFICATION SUMMARY DATE: 09/06/2006
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Input Set : **E:\DJKIM.GENO.PT2.ST25.txt**
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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date